

Amendment to the Claims:

Please amend the claims as follows.

Please cancel claims 218 and 221 to 240, without prejudice of disclaimer.

This listing of claims will replace all prior versions, and listing, of claims in the application:

Listing of Claims:

Claims 1 to 215 (canceled)

Claim 216 (currently amended): A method for making a composition ~~to treat a wood, a wood product, a wood pulp, a Kraft pulp, a paper, a paper product, a paper pulp, or a combination thereof,~~ comprising

(i) (a) providing a carrier;

(b) providing a polypeptide having a xylanase activity ~~which is active under conditions comprising a temperature of at least 85°C and a basic pH of at least pH 11, and~~

(c) combining the carrier of (a) with the polypeptide xylanase of (b);

~~thereby producing a composition to treat a wood, a wood product, a wood pulp, a Kraft pulp, a paper, a paper product, a paper pulp, or a combination thereof;~~

wherein the polypeptide having a xylanase activity has at least about 90% sequence identity to SEQ ID NO:160, or an enzymatically active fragment thereof; or

(ii) the method of (i), wherein the sequence comparison algorithm is a BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F F, and all other options are set to default.

Claim 217 (currently amended): A method for making a composition ~~to treat a wood, a wood product, a wood pulp, a Kraft pulp, a paper, a paper product, a paper pulp, or a combination thereof, wherein the composition comprises a xylanase that is active under high temperature of at least 80°C and basic pH conditions of at least pH 10.5,~~ comprising

(a) providing a carrier appropriate for temperatures of at least 80°C;

(b) providing a polypeptide having a ~~[[the]]~~ xylanase activity that is active under high temperature of at least 80°C and ~~basic pH conditions of at least pH 10.5,~~ and having at least about 90% sequence identity to SEQ ID NO:160; and

(c) combining the carrier of (a) with the polypeptide ~~xylanase~~ of (b),
thereby producing the composition.

Claim 218 (canceled)

Claim 219 (currently amended): The method of claim 216 ~~or claim 217,~~ wherein the polypeptide having a xylanase activity ~~comprises~~

(a) — (i) ~~a nucleic acid encoding at least one polypeptide having a xylanase activity, wherein the nucleic acid comprises a sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or has 100% sequence identity to SEQ ID NO:159; or~~

(ii) ~~a nucleic acid encoding at least one polypeptide having a xylanase activity, wherein the nucleic acid comprises a sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or has 100% sequence identity to SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID~~

~~NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379, over a region of at least about 50, 75, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150 or more residues, or the full length of a gene or a transcript, or~~

(iii) the nucleic acid of (i) or (ii), wherein the sequence comparison algorithm is a ~~BLAST version 2.2.2 algorithm where a filtering setting is set to blastall -p blastp -d "nr pataa" -F~~, and all other options are set to default;

(b) — a nucleic acid encoding at least one polypeptide having a xylanase activity, wherein the nucleic acid comprises

(i) a sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence of SEQ ID NO:159,

(ii) a sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence of ~~SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:199, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID~~

~~NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, SEQ ID NO:233, SEQ ID NO:235, SEQ ID NO:237, SEQ ID NO:239, SEQ ID NO:241, SEQ ID NO:243, SEQ ID NO:245, SEQ ID NO:247, SEQ ID NO:249, SEQ ID NO:251, SEQ ID NO:253, SEQ ID NO:255, SEQ ID NO:257, SEQ ID NO:259, SEQ ID NO:261, SEQ ID NO:263, SEQ ID NO:265, SEQ ID NO:267, SEQ ID NO:269, SEQ ID NO:271, SEQ ID NO:273, SEQ ID NO:275, SEQ ID NO:277, SEQ ID NO:279, SEQ ID NO:281, SEQ ID NO:283, SEQ ID NO:285, SEQ ID NO:287, SEQ ID NO:289, SEQ ID NO:291, SEQ ID NO:293, SEQ ID NO:295, SEQ ID NO:297, SEQ ID NO:299, SEQ ID NO:301, SEQ ID NO:303, SEQ ID NO:305, SEQ ID NO:307, SEQ ID NO:309, SEQ ID NO:311, SEQ ID NO:313, SEQ ID NO:315, SEQ ID NO:317, SEQ ID NO:319, SEQ ID NO:321, SEQ ID NO:323, SEQ ID NO:325, SEQ ID NO:327, SEQ ID NO:329, SEQ ID NO:331, SEQ ID NO:333, SEQ ID NO:335, SEQ ID NO:337, SEQ ID NO:339, SEQ ID NO:341, SEQ ID NO:343, SEQ ID NO:345, SEQ ID NO:347, SEQ ID NO:349, SEQ ID NO:351, SEQ ID NO:353, SEQ ID NO:355, SEQ ID NO:357, SEQ ID NO:359, SEQ ID NO:361, SEQ ID NO:363, SEQ ID NO:365, SEQ ID NO:367, SEQ ID NO:369, SEQ ID NO:371, SEQ ID NO:373, SEQ ID NO:375, SEQ ID NO:377 or SEQ ID NO:379,~~

~~(iii) the nucleic acid of (i) or (ii), wherein the stringent conditions comprise a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes, or~~

~~(iv) the nucleic acid of (i) or (ii), wherein the nucleic acid is at least about 50, 75, 100, 150, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more residues in length or the full length of the gene or transcript;~~

~~(e) — a nucleic acid encoding a polypeptide having xylanase activity, wherein the polypeptide comprises~~

~~(i) the amino acid sequence of SEQ ID NO:160, or~~

~~(ii) the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ~~

~~ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID~~

~~NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380, or enzymatically active fragments thereof;~~

~~(d) — a nucleic acid encoding a polypeptide having xylanase activity made by a method comprising:~~

~~(a) (i) providing a template nucleic acid comprising the nucleic acid sequence of (a), (b) or (c); (ii) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid; and (iii) expressing the variant of the template nucleic acid to generate a recombinant polypeptide and testing the recombinant polypeptide for xylanase activity; or~~

~~(b) (i) providing a template nucleic acid comprising the nucleic acid sequence of (a), (b) or (c) encoding a polypeptide having a xylanase activity; and, (ii) modifying, deleting or adding one or more nucleotides in the template sequence, or a combination thereof, to generate a variant of the template nucleic acid, wherein the variant nucleic acid encodes a polypeptide that retains xylanase activity under conditions comprising a temperature of at least about 70°C, 80°C or 90°C or more, and a basic pH of at least about pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5, pH 11 or more,~~

~~wherein optionally the modifications, additions or deletions are introduced by a method comprising error prone PCR, shuffling, oligonucleotide directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof; or~~

~~(iii) the nucleic acid of (i) or (ii), wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate modified DNA mutagenesis, uracil containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-~~

~~selection mutagenesis, restriction purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof;~~

~~(e) — the nucleic acid of (a), (b), (c) or (d) encoding a xylanase but lacking a signal sequence or carbohydrate binding module;~~

~~(f) — the nucleic acid of (a), (b), (c), (d) or (e) encoding a xylanase but having a heterologous sequence, wherein optionally the heterologous sequence comprises a heterologous signal sequence, carbohydrate binding module, catalytic domain (CD), or a combination thereof, and optionally the heterologous signal sequence, carbohydrate binding module or catalytic domain (CD) is derived from another xylanase or a non-xylanase enzyme;~~

~~(g) — a nucleic acid comprising a sequence complementary to (a), (b), (c), (d), (e) or (f);~~

~~(h) — wherein the xylanase of (a), (b), (c), (d), (e), or (f) **retains activity under conditions comprising a temperature of at least about 80°C** 85°C and a basic pH of at least about pH 11;~~

~~(i) — wherein the xylanase activity of (a), (b), (c), (d), (e), (f) or (g) comprises catalyzing hydrolysis of internal β -1,4 xylosidic linkages; an endo-1,4 beta-xylanase activity; hydrolyzing a xylan, an arabinoxylan or a water-soluble arabinoxylan to produce a smaller molecular weight xylose and xylo-oligomer; hydrolyzing a xylan, an arabinoxylan or a water-soluble arabinoxylan in a dough or a bread product; hydrolyzing polysaccharides comprising 1,4 β -glycoside-linked D-xylopyranoses; hydrolyzing hemicelluloses; hydrolyzing hemicelluloses in a wood, a wood product, a wood pulp, a Kraft pulp, a paper pulp, a paper, a paper product, or a combination thereof; catalyzing hydrolysis of xylans in a feed or a food product, or a food, feed or nutritional supplement; catalyzing hydrolysis of xylans in a cereal-based animal food or feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable; catalyzing hydrolysis of xylans in a microbial cell or a plant cell;~~

~~(j) — wherein the xylanase activity of (a), (b), (c), (d), (e), (f), (g) or (h) is thermostable, or the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C;~~

~~(k) — wherein the xylanase activity of (a), (b), (c), (d), (e), (f), (g) or (h) is thermotolerant, or the polypeptide retains a xylanase activity after exposure to a temperature in the range from~~

greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C; or

(l) — wherein the polypeptide of any of (a) to (k) retains a xylanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0, or the polypeptide retains a xylanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.

Claim 220 (currently amended): The method of claim 216 ~~or claim 217~~, wherein the xylanase comprises

(a) — a polypeptide having xylanase activity, ~~wherein the polypeptide comprises an amino acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or has 100% sequence identity to the amino acid sequence of SEQ ID NO:160,~~

(b) — a polypeptide having xylanase activity, ~~wherein the polypeptide comprises an amino acid sequence having at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or has 100% sequence identity to the amino acid sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108,~~

~~SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132; SEQ ID NO:134; SEQ ID NO:136; SEQ ID NO:138; SEQ ID NO:140; SEQ ID NO:142; SEQ ID NO:144; NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, SEQ ID NO:234, SEQ ID NO:236, SEQ ID NO:238, SEQ ID NO:240, SEQ ID NO:242, SEQ ID NO:244, SEQ ID NO:246, SEQ ID NO:248, SEQ ID NO:250, SEQ ID NO:252, SEQ ID NO:254, SEQ ID NO:256, SEQ ID NO:258, SEQ ID NO:260, SEQ ID NO:262, SEQ ID NO:264, SEQ ID NO:266, SEQ ID NO:268, SEQ ID NO:270, SEQ ID NO:272, SEQ ID NO:274, SEQ ID NO:276, SEQ ID NO:278, SEQ ID NO:280, SEQ ID NO:282, SEQ ID NO:284, SEQ ID NO:286, SEQ ID NO:288, SEQ ID NO:290, SEQ ID NO:292, SEQ ID NO:294, SEQ ID NO:296, SEQ ID NO:298, SEQ ID NO:300, SEQ ID NO:302, SEQ ID NO:304, SEQ ID NO:306, SEQ ID NO:308, SEQ ID NO:310, SEQ ID NO:312, SEQ ID NO:314, SEQ ID NO:316, SEQ ID NO:318, SEQ ID NO:320, SEQ ID NO:322, SEQ ID NO:324, SEQ ID NO:326, SEQ ID NO:328, SEQ ID NO:330, SEQ ID NO:332, SEQ ID NO:334, SEQ ID NO:336, SEQ ID NO:338, SEQ ID NO:340, SEQ ID NO:342, SEQ ID NO:344, SEQ ID NO:346, SEQ ID NO:348, SEQ ID NO:350, SEQ ID NO:352, SEQ ID NO:354, SEQ ID NO:356, SEQ ID NO:358, SEQ ID NO:360, SEQ ID NO:362, SEQ ID NO:364, SEQ ID NO:366, SEQ ID NO:368, SEQ ID NO:370, SEQ ID NO:372, SEQ ID NO:374, SEQ ID NO:376, SEQ ID NO:378 or SEQ ID NO:380, over a region of at least about 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 250, 300 or more residues, or over the full length of the polypeptide;~~

(c) — ~~the polypeptide of (a) or (b), wherein the sequence identities are determined by analysis with a sequence comparison algorithm or by a visual inspection;~~

~~(d) — a polypeptide having xylanase activity, wherein the polypeptide comprises an amino acid sequence encoded by a nucleic acid having a sequence as set forth in claim 219;~~

~~(e) — a polypeptide made by a method comprising:~~

~~providing a template sequence comprising the amino acid sequence of (a) or (b);~~

~~(ii) modifying, deleting or adding one or more amino acids in the template sequence, or a combination thereof, to generate a variant of the template sequence; and (iii) expressing the variant of the template sequence to generate a recombinant polypeptide and testing the recombinant polypeptide for xylanase activity;~~

~~wherein optionally the polypeptide that retains xylanase activity under conditions comprising a temperature of at least about 70°C, 80°C or 90°C or more, and a basic pH of at least about pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10, pH 10.5, pH 11 or more,~~

~~and optionally the modifications, additions or deletions are introduced by a method comprising error-prone PCR, shuffling, oligonucleotide-directed mutagenesis, assembly PCR, sexual PCR mutagenesis, *in vivo* mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, Gene Site Saturation Mutagenesis (GSSM), synthetic ligation reassembly (SLR) and a combination thereof;~~

~~and optionally wherein the modifications, additions or deletions are introduced by a method comprising recombination, recursive sequence recombination, phosphothioate-modified DNA mutagenesis, uracil-containing template mutagenesis, gapped duplex mutagenesis, point mismatch repair mutagenesis, repair-deficient host strain mutagenesis, chemical mutagenesis, radiogenic mutagenesis, deletion mutagenesis, restriction-selection mutagenesis, restriction-purification mutagenesis, artificial gene synthesis, ensemble mutagenesis, chimeric nucleic acid multimer creation and a combination thereof;~~

~~(f) — the polypeptide of any of (a) to (e), but lacking a signal sequence or carbohydrate binding module; or~~

~~(g) — the polypeptide of any of (a) to (f), and having a heterologous sequence, wherein optionally the heterologous sequence comprises a heterologous signal sequence, carbohydrate binding module, catalytic domain (CD), or a combination thereof, wherein optionally the~~

heterologous signal sequence, carbohydrate binding module or catalytic domain (CD) is derived from another xylanase or a non-xylanase enzyme;

(h) — the polypeptide of any of (a) to (g), wherein the xylanase of (a), (b), (c) or (d) retains activity under conditions comprising a temperature of at least about 85°C and a basic pH of at least about pH 11;

(i) — the polypeptide of any of (a) to (h), wherein the xylanase activity comprises catalyzing hydrolysis of internal β 1,4 xylosidic linkages; an endo 1,4 beta xylanase activity; hydrolyzing a xylan, an arabinoxylan or a water soluble arabinoxylan to produce a smaller molecular weight xylose and xylo oligomer; hydrolyzing a xylan, an arabinoxylan or a water soluble arabinoxylan in a dough or a bread product; hydrolyzing polysaccharides comprising 1,4- β -glycoside linked D xylopyranoses; hydrolyzing hemicelluloses; hydrolyzing hemicelluloses in a wood, a wood product, a wood pulp, a Kraft pulp, a paper pulp, a paper, a paper product, or a combination thereof; catalyzing hydrolysis of xylans in a feed or a food product, or a food, feed or nutritional supplement; catalyzing hydrolysis of xylans in a cereal based animal food or feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable; catalyzing hydrolysis of xylans in a microbial cell or a plant cell;

(j) — the polypeptide of any of (a) to (i), wherein the xylanase activity is thermostable, or the polypeptide retains a xylanase activity under conditions comprising a temperature range of between about 37°C to about 95°C, or between about 55°C to about 85°C, or between about 70°C to about 75°C, or between about 70°C to about 95°C, or between about 90°C to about 95°C;

(k) — the polypeptide of any of (a) to (i), wherein the xylanase activity is thermotolerant, or the polypeptide retains a xylanase activity after exposure to a temperature in the range from greater than 37°C to about 95°C, from greater than 55°C to about 85°C, or between about 70°C to about 75°C, or from greater than 90°C to about 95°C;

(l) — the polypeptide of any of (a) to (i), wherein the xylanase activity comprises a specific activity at about 37°C in the range from about 100 to about 1000 units per milligram of protein, from about 500 to about 750 units per milligram of protein, from about 500 to about 1200 units per milligram of protein, or from about 750 to about 1000 units per milligram of protein;

~~(m) — the polypeptide of any of (k), wherein the thermotolerance comprises retention of at least half of the specific activity of the xylanase at 37°C after being heated to an elevated temperature;~~

~~(n) — the polypeptide of any of (k), wherein the thermotolerance comprises retention of specific activity at 37°C in the range from about 500 to about 1200 units per milligram of protein after being heated to an elevated temperature;~~

~~(o) — the polypeptide of any of (a) to (n), wherein the polypeptide comprises at least one glycosylation site, and optionally the glycosylation is an N linked glycosylation, or the polypeptide is glycosylated after being expressed in a *P. pastoris* or a *S. pombe*; or~~

~~(p) — the polypeptide of any of (a) to (o), wherein the polypeptide retains a xylanase activity under conditions comprising about pH 6.5, pH 6.0, pH 5.5, 5.0, pH 4.5 or 4.0, or the polypeptide retains a xylanase activity under conditions comprising about pH 7.5, pH 8.0, pH 8.5, pH 9, pH 9.5, pH 10 or pH 10.5.~~

Claims 221 to 240 (canceled)

Claim 241 (new): The method of claim 216, wherein the method for making a composition comprises providing a carrier appropriate for making a composition for treating a wood, a wood product, a wood pulp, a Kraft pulp, a paper, a paper product, a paper pulp, or a combination thereof.

Claim 242 (new): A method for making a composition comprising

- (a) providing a carrier;
- (b) providing a polypeptide having a xylanase activity, and
- (c) combining the carrier of (a) with the polypeptide of (b);

wherein the polypeptide is encoded by a nucleic acid having a sequence that hybridizes under stringent conditions to a nucleic acid comprising the sequence of SEQ ID NO:159, wherein the stringent conditions comprise a wash step comprising a wash in 0.2X SSC at a temperature of about 65°C for about 15 minutes.

Claim 243 (new): The method of claim 219, wherein the polypeptide having a xylanase activity has at least about 94% sequence identity to SEQ ID NO:160.

Claim 244 (new): The method of claim 243, wherein the polypeptide having a xylanase activity has at least about 96% sequence identity to SEQ ID NO:160.

Claim 245 (new): The method of claim 244, wherein the polypeptide having a xylanase activity has at least about 98% sequence identity to SEQ ID NO:160.

Claim 246 (new): The method of claim 245, wherein the polypeptide having a xylanase activity has 100% (complete) sequence identity to SEQ ID NO:160.

Claim 247 (new): The method of claim 242, wherein the polypeptide having a xylanase activity has at least about 94% sequence identity to SEQ ID NO:160.

Claim 248 (new): The method of claim 247, wherein the polypeptide having a xylanase activity has at least about 96% sequence identity to SEQ ID NO:160.

Claim 249 (new): The method of claim 248, wherein the polypeptide having a xylanase activity has at least about 98% sequence identity to SEQ ID NO:160.

Claim 250 (new): The method of claim 249, wherein the polypeptide having a xylanase activity has 100% (complete) sequence identity to SEQ ID NO:160.

Claim 251 (new): The method of claim 216, wherein the polypeptide lacks an endogenous signal sequence and/or carbohydrate binding module.

Claim 252 (new): The method of claim 216, wherein the polypeptide further comprises a heterologous polypeptide sequence.

Claim 253 (new): The method of claim 216, wherein the polypeptide lacks an endogenous signal sequence and further comprises a heterologous signal sequence.

Claim 254 (new): The method of claim 252, wherein the heterologous sequence comprises a heterologous signal sequence, a carbohydrate binding module, a catalytic domain (CD), or a combination thereof.

Claim 255 (new): The method of claim 254, wherein the heterologous signal sequence, carbohydrate binding module or catalytic domain (CD) is derived from a xylanase or a non-xylanase enzyme.

Claim 256 (new): The method of claim 216, wherein the xylanase activity comprises catalyzing hydrolysis of internal β -1,4-xylosidic linkages.

Claim 257 (new): The method of claim 216, wherein the xylanase activity comprises an endo-1,4-beta-xylanase activity.

Claim 258 (new): The method of claim 216, wherein the xylanase activity comprises hydrolyzing a xylan, an arabinoxylan or a water soluble arabinoxylan to produce a smaller molecular weight xylose and xylo-oligomer.

Claim 259 (new): The method of claim 216, wherein the xylanase activity comprises hydrolyzing a xylan, an arabinoxylan or a water soluble arabinoxylan in a dough or a bread product.

Claim 260 (new): The method of claim 216, wherein the xylanase activity comprises hydrolyzing polysaccharides comprising 1,4- β -glycoside-linked D-xylopyranoses.

Claim 261 (new): The method of claim 216, wherein the xylanase activity comprises hydrolyzing hemicelluloses.

Claim 262 (new): The method of claim 261, wherein the xylanase activity comprises hydrolyzing hemicelluloses in a wood, a wood product, a wood pulp, a Kraft pulp, a paper pulp, a paper, a paper product, or a combination thereof.

Claim 263 (new): The method of claim 216, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a feed or a food product, or a food, feed or nutritional supplement.

Claim 264 (new): The method of claim 216, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a cereal-based animal food or feed, a wort or a beer, a milk or a milk product, a fruit or a vegetable.

Claim 265 (new): The method of claim 216, wherein the xylanase activity comprises catalyzing hydrolysis of xylans in a microbial cell or a plant cell.